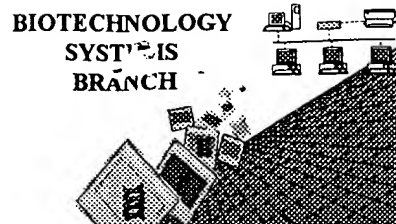


1648 # 10



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/757,655
Source: 1600
Date Processed by STIC: 2/21/2002

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Application No.: 09/757,655

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002

TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

Does Not Comply
Corrected Diskette Needed

pg 1-5

3 <110> APPLICANT: FUJII, Takeru
 4 YOKOYAMA, Hideakira
 5 HAMAMOTO, Hidetoshi
 7 <120> TITLE OF INVENTION: A PEPTIDE HAVING AN AFFINITY FOR gp120
 9 <130> FILE REFERENCE: 2001-0019A/LC/01732
 11 <140> CURRENT APPLICATION NUMBER: 09/757,655
 12 <141> CURRENT FILING DATE: 2001-01-11
 14 <150> PRIOR APPLICATION NUMBER: JP No. 2000-6182
 15 <151> PRIOR FILING DATE: 2000-01-11
 17 <160> NUMBER OF SEQ ID NOS: 19
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
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 23 <212> TYPE: PRT
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 27 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
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 31 <222> LOCATION: (1)
 32 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr
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 41 <222> LOCATION: (3)
 42 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
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 52 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
 Lys, Arg,
 53 Phe, Trp, Pro or Tyr
 55 <400> SEQUENCE: 1
 56 Xaa Xaa Xaa Xaa Xaa
 57 1 5
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 5

insufficient explanation -
 give source
 of genetic
 material
 (see item 11
 on Error
 Summary
 sheet)

RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/757,655

TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

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 70 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr, or polypeptide residue that an
 71 arbitrary amino acid stood in line in the N-terminal side from this amino acid
 73 <220> FEATURE:

W--> 74 <221> NAME/KEY: Residue
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 76 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
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 92 Phe, Trp, Pro or Tyr
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002
TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

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128 <222> LOCATION: (5)
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Arg,
130 Phe, Trp, Pro or Tyr, or polypeptide residue that an arbitrary amino acid
131 stood in line in the C-terminal side of this amino acid, H
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135 1 5
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161 <220> FEATURE:
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165 Phe or Trp
167 <220> FEATURE:
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RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/757,655

TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

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 187 <222> LOCATION: (1)
 188 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp, or polypeptide residue that an
 189 arbitrary amino acid stood in the N-terminal side from this amino acid
 191 <220> FEATURE:

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 193 <222> LOCATION: (2)
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 205 Phe or Trp
 207 <220> FEATURE:

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 209 <222> LOCATION: (5)
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 211 Phe, Tyr or Trp

W--> 213 <400> SEQUENCE: 5
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 215 1 5
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 235 <220> FEATURE:

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 244 Phe or Trp
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RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/757,655

TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

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Lys, Arg,
250 Phe, Tyr or Trp, or polypeptide residue that an arbitrary amino acid stood in
line
251 in the C-terminal side of this amino acid
253 <400> SEQUENCE: 6/
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255 1 5
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307 <212> TYPE: PRT
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:

*Please correct
this error in
subsequent sequences*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002

TIME: 11:38:42

Input Set : A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

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L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
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L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
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L:127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
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L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:186 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
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L:202 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
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L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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L:247 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

RECEIVED

MAR 08 2002

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/757,655

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(ix) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001